

FIGURE 1**Target segment starts with AA**

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
AAGATCCTCAAGAATGACGCC [SEQ ID NO:18]	0.48	117	GAUCCUCAAGAAUGACGCCUU [SEQ ID NO:35] UUCUAGGAGUUCUUACUGCGG [SEQ ID NO:52]
AAGAATGACGCCTACCGCAAC [SEQ ID NO:19]	0.52	126	GAAUGACGCCUACCGCAACUU [SEQ ID NO:36] UUCUUACUGCGGAUGGCGUUG [SEQ ID NO:53]
AACCGCATCATCAAGAACGAG [SEQ ID NO:20]	0.48	144	CCGCAUCAUCAAGAACGAGUU [SEQ ID NO:37] UUGGCGUAGUAGUUCUUGCUC [SEQ ID NO:54]
AAGAACGAGCTGAAGCTGCTG [SEQ ID NO:21]	0.52	156	GAACGAGCUGAAGCUGCUGUU [SEQ ID NO:38] UUCUUGCUCGACUUCGACGAC [SEQ ID NO:55]
AAGGAGCTGGCTATCATCCAC [SEQ ID NO:22]	0.52	381	GGAGCUGGCUAUCAUCCACUU [SEQ ID NO:39] UUCCUCGACCGAUAGUAGGUG [SEQ ID NO:56]
AAGCCTGAGAACATCATGCTG [SEQ ID NO:23]	0.48	411	GCCUGAGAACAUCAUGCUGUU [SEQ ID NO:40] UUCGGACUCUUGUAGUACGAC [SEQ ID NO:57]
AACATCATGCTGGTGGACCAG [SEQ ID NO:24]	0.52	420	CAUCAUGCUGGUGGACCAGUU [SEQ ID NO:41] UUGUAGUACGACCACCUGGUC [SEQ ID NO:58]
AAGGTGATTGACTTCGGATCC [SEQ ID NO:25]	0.48	462	GGUGAUUGACUUCGGAUCCUU [SEQ ID NO:42] UUCCACUACUGAAGCCUAGG [SEQ ID NO:59]
AAGGAGCCATACATCCAGTCG [SEQ ID NO:26]	0.52	513	GGAGCCAUACAUCCAGUCGUU [SEQ ID NO:43] UUCCUCGGUAGUAGGUCAGC [SEQ ID NO:60]

AACAACGAGTACGACCAGGTG [SEQ ID NO:27]	0.52	651	CAACGAGUACGACCAGGUGUU [SEQ ID NO:44] UUGUUGCUCUAGCUGGUCCAC [SEQ ID NO:61]
AAGTCGTTGGACCAGATTGAG [SEQ ID NO:28]	0.48	855	GUCGUUGGACCAGAUUGAGUU [SEQ ID NO:45] UUCAGCAACCUGGUCUAAACUC [SEQ ID NO:62]
AAGAGCATGGTGGAGCTGATC [SEQ ID NO:29]	0.52	951	GAGCAUGGUGGAGCUGAUCUU [SEQ ID NO:46] UUCUCGUACCACCUCGACUAG [SEQ ID NO:63]
AATGCGGTCTCCGACATGATG [SEQ ID NO:30]	0.52	1341	UGCGGUCUCCGACAUGAUGUU [SEQ ID NO:47] UUACGCCAGAGGCUGUACUAC [SEQ ID NO:64]
AAGTCCGACTCCAACCTCAGC [SEQ ID NO:31]	0.52	1485	GUCCGACUCCAACUUCAGCUU [SEQ ID NO:48] UUCAGGCUGAGGUUGAAGUCG [SEQ ID NO:65]
AACTTCAGCAACCTCATTCGG [SEQ ID NO:32]	0.48	1497	CUUCAGCAACCUCAUUCGGUU [SEQ ID NO:49] UUGAAGUCGUUGGAGUAAAGCC [SEQ ID NO:66]
AACATGACCATGGAAGCTGAG [SEQ ID NO:33]	0.48	1647	CAUGACCAUGGAAGCUGAGUU [SEQ ID NO:50] UUGUACUGGUACCUUCGACUC [SEQ ID NO:67]
AATGGCTGAGTGAGCCAGACT [SEQ ID NO:34]	0.52	1711	UGGCUGAGUGAGCCAGACUUU [SEQ ID NO:51] UUACCGACUCACUCGGUCUGA [SEQ ID NO:68]

Target segment starts with CA

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
CAAGATCCTCAAGAATGACGC [SEQ ID NO:69]	0.48	116	AGAUCCUCAAGAAUGACGCUU [SEQ ID NO:89] UUUCUAGGAGUUCUACUGCG [SEQ ID NO:109]
CAAGAATGACGCCTACCGCAA [SEQ ID NO:70]	0.52	125	AGAAUGACGCCUACCGCAAUU [SEQ ID NO:90] UUUCUUACUGCGGAUGGCGUU [SEQ ID NO:110]

CAACCGCATCATCAAGAACGA [SEQ ID NO:71]	0.48	143	ACCGCAUCAUCAAGAACGAUU [SEQ ID NO:91] UUUGGCGUAGUAGUUCUUGCU [SEQ ID NO:111]
CATCAAGAACGAGCTGAAGCT [SEQ ID NO:72]	0.48	152	UCAAGAACGAGCUGAAGCUUU [SEQ ID NO:92] UUAGUUCUUGCUCGACUUCGA [SEQ ID NO:112]
CAAGAACGAGCTGAAGCTGCT [SEQ ID NO:73]	0.52	155	AGAACGAGCUGAAGCUGCUUU [SEQ ID NO:93] UUUCUUGCUCGACUUCGACGA [SEQ ID NO:113]
CATCCGCTTCCTTGAGTTCTT [SEQ ID NO:74]	0.48	215	UCCGCUUCCUUGAGUUCUUUU [SEQ ID NO:94] UUAGGCGAAGGAACUCAAGAA [SEQ ID NO:114]
CAGAAGGAGAACAACCTTCGCG [SEQ ID NO:75]	0.52	297	GAAGGAGAACAACUUCGCGUU [SEQ ID NO:95] UUCUCCUCUUGUUGAAGCGC [SEQ ID NO:115]
CAAGGAGCTGGCTATCATCCA [SEQ ID NO:76]	0.52	380	AGGAGCUGGCUAUCAUCCAUU [SEQ ID NO:96] UUUCCUCGACCGAUAGUAGGU [SEQ ID NO:116]
CAAGCCTGAGAACATCATGCT [SEQ ID NO:77]	0.48	410	AGCCUGAGAACAUCAUGCUUU [SEQ ID NO:97] UUUCGGACUCUUGUAGUACGA [SEQ ID NO:117]
CAAGGTGATTGACTTCGGATC [SEQ ID NO:78]	0.48	461	AGGUGAUUGACUUCGGAUCUU [SEQ ID NO:98] UUUCCACUAACUGAAGCCUAG [SEQ ID NO:118]
CATACATCCAGTCGCGCTTCT [SEQ ID NO:79]	0.52	520	UACAUCCAGUCGCGCUUCUUU [SEQ ID NO:99] UUAUGUAGGUCAGCGCGAAGA [SEQ ID NO:119]
CAACAACGAGTACGACCAGGT [SEQ ID NO:80]	0.52	650	ACAACGAGUACGACCAGGUUU [SEQ ID NO:100] UUUGUUGCUCUUGCUGGUCCA [SEQ ID NO:120]
CACCACTTCTTCAAGCGCAAC [SEQ ID NO:81]	0.52	735	CCACUUCUUAAGCGCAACUU [SEQ ID NO:101] UUGGUGAAGAAGUUCGCGUUG [SEQ ID NO:121]

CAAGTCGTTGGACCAGATTGA [SEQ ID NO:82]	0.48	854	AGUCGUUGGACCAGAUUGAUU [SEQ ID NO:102] UUUCAGCAACCUUGGUCUAACU [SEQ ID NO:122]
CAAGAGCATGGTGGAGCTGAT [SEQ ID NO:83]	0.52	950	AGAGCAUGGUGGAGCUGAUUU [SEQ ID NO:103] UUUCUCGUACCACCUCGACUA [SEQ ID NO:123]
CAATGCGGTCTCCGACATGAT [SEQ ID NO:84]	0.52	1340	AUGCGGUCUCCGACAUGAUUU [SEQ ID NO:104] UUUACGCCAGAGGCUGUACUA [SEQ ID NO:124]
CAAGTCCGACTCCAACCTCAG [SEQ ID NO:85]	0.52	1484	AGUCCGACUCCAACUUCAGUU [SEQ ID NO:105] UUUCAGGCUGAGGUUGAAGUC [SEQ ID NO:125]
CAACTTCAGCAACCTCATTCG [SEQ ID NO:86]	0.48	1496	ACUUCAGCAACCUCAUUCGUU [SEQ ID NO:106] UUUGAAGUCGUUGGAGUAAGC [SEQ ID NO:126]
CAACATGACCATGGAAGCTGA [SEQ ID NO:87]	0.48	1646	ACAUGACCAUGGAAGCUGAUU [SEQ ID NO:107] UUUGUACUGGUACCUUCGACU [SEQ ID NO:127]
CATGACCATGGAAGCTGAGAG [SEQ ID NO:88]	0.52	1649	UGACCAUGGAAGCUGAGAGUU [SEQ ID NO:108] UUACUGGUACCUUCGACUCUC [SEQ ID NO:128]

Target segment starts with GA

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
GAGATGGTGGCCATCAAGATC [SEQ ID NO:129]	0.52	102	GAUGGUGGCCAUCAAGAUCUU [SEQ ID NO:144] UUCUACCACCGGUAGUUCUAG [SEQ ID NO:159]
GATGGTGGCCATCAAGATCCT [SEQ ID NO:130]	0.52	104	UGGUGGCCAUCAAGAUCUUU [SEQ ID NO:145] UUACCACCGGUAGUUCUAGGA [SEQ ID NO:160]
GATCCTCAAGAATGACGCCTA [SEQ ID NO:131]	0.48	119	UCCUCAAGAAUGACGCCUAUU [SEQ ID NO:146] UUAGGAGUUCUUACUGCGGAU [SEQ ID NO:161]

GAGTTCCAGAAGGAGAACAAC [SEQ ID NO:132]	0.48	291	GUUCCAGAAGGAGAACAACUU [SEQ ID NO:147] UUCAAGGUCUCCUCUUGUUG [SEQ ID NO:162]
GATCTCAAGCCTGAGAACATC [SEQ ID NO:133]	0.48	405	UCUCAAGCCUGAGAACAUCUU [SEQ ID NO:148] UUAGAGUUCGGACUCUUGUAG [SEQ ID NO:163]
GAGAACATCATGCTGGTGGAC [SEQ ID NO:134]	0.52	417	GAACAUCAUGCUGGUGGACUU [SEQ ID NO:149] UUCUUGUAGUACGACCACCUG [SEQ ID NO:164]
GAACATCATGCTGGTGGACCA [SEQ ID NO:135]	0.52	419	ACAUCAUGCUGGUGGACCAUU [SEQ ID NO:150] UUUGUAGUACGACCACCUGGU [SEQ ID NO:165]
GAAGGAGCCATACATCCAGTC [SEQ ID NO:136]	0.52	512	AGGAGCCAUACAUCAGUCUU [SEQ ID NO:151] UUUCCUCGGUAUGUAGGUCAG [SEQ ID NO:166]
GATTGAGACAGTGAATGGTGG [SEQ ID NO:137]	0.48	869	UUGAGACAGUGAAUGGUGGUU [SEQ ID NO:152] UUAACUCUGUCACUUACCACC [SEQ ID NO:167]
GAGACAGTGAATGGTGGCAGT [SEQ ID NO:138]	0.52	873	GACAGUGAAUGGUGGCAGUUU [SEQ ID NO:153] UUCUGUCACUUACCACCGUCA [SEQ ID NO:168]
GACAGTGAATGGTGGCAGTGT [SEQ ID NO:139]	0.52	875	CAGUGAAUGGUGGCAGUGUUU [SEQ ID NO:154] UUGUCACUUACCACCGUCACA [SEQ ID NO:169]
GAGCATGGTGGAGCTGATCAA [SEQ ID NO:140]	0.52	953	GCAUGGUGGAGCUGAUCAAUU [SEQ ID NO:155] UUCGUACCACCUCGACUAGUU [SEQ ID NO:170]
GAGAAGGCACCAGGTATGCAA [SEQ ID NO:141]	0.52	1248	GAAGGCACCAGGUAUGCAAUU [SEQ ID NO:156] UUCUCCGUGGUCCAUACGUU [SEQ ID NO:171]
GACTCCAACCTTCAGCAACCTC [SEQ ID NO:142]	0.52	1491	CUCCAACUUCAGCAACCUCUU [SEQ ID NO:157] UUGAGGUUGAAGUCGUUGGAG [SEQ ID NO:172]

GACAACATGACCATGGAAGCT [SEQ ID NO:143]	0.48	1644	CAACAUGACCAUGGAAGCUUU [SEQ ID NO:158] UUGUUGUACUGGUACCUUCGA [SEQ ID NO:173]
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Target segment starts with TA

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
TACCGCAACCGCATCATCAAG [SEQ ID NO:174]	0.52	138	CCGCAACCGCAUCAUCAAGUU [SEQ ID NO:180] UUGGCGUUGGCGUAGUAGUUC [SEQ ID NO:186]
TACGTGAAGGAGCCATACATC [SEQ ID NO:175]	0.48	507	CGUGAAGGAGCCAUACAUCUU [SEQ ID NO:181] UUGCACUCCUCGGUAUGUAG [SEQ ID NO:187]
TACATCCAGTCGCGCTTCTAC [SEQ ID NO:176]	0.52	522	CAUCCAGUCGCGCUUCUACUU [SEQ ID NO:182] UUGUAGGUCAGCGCAAGAUG [SEQ ID NO:188]
TATGCTCAAGTCGTTGGACCA [SEQ ID NO:177]	0.48	848	UGCUC AAGUCGUUGGACCAUU [SEQ ID NO:183] UUACGAGUUCAGCAACCUGGU [SEQ ID NO:189]
TACTACTGTCTGGCTGAGGAG [SEQ ID NO:178]	0.52	1173	CUACUGUCUGGCUGAGGAGUU [SEQ ID NO:184] UUGAUGACAGACCGACUCCUC [SEQ ID NO:190]
TACTGTCTGGCTGAGGAGAAG [SEQ ID NO:179]	0.52	1176	CUGUCUGGCUGAGGAGAAGUU [SEQ ID NO:185] UUGACAGACCGACUCCUCUUC [SEQ ID NO:191]

FIGURE 2

A

Protein Sequence of Human HIPK4

Total length -- 616 AA

MSTIQSETDCYDIIIEVLGKGTGFEVAKGWRRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFH
DALKFYLVFELLEQNLFQKNNFAPLPAHIRTVTLQVLTALARLKEIAIHADLKPENIMLVDQTRCPFRVKVIDFG
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH
AACKAHFFFKRNPHPDAAANPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSSVASRLTFPDREALAEHADLKSM
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHETTHYYQLSLRSYRLSLQVEGKPPTPVVAAEDGTPYYCLAEKE
AAGMGSVAGSSPFFREEKAPGMQRAIDQLDDLSLQEAGHGLWGETCTNAVSDMMVPLKAAITGHHVPDSGPEPILAFYSS
RLAGRHKARKPPAGSKSDSNFSNLIRLSQVSPEDDRPCRGSSWEEGHLGASAEPLAILQRDEDGPNIDNMTMEAERPDP
ELFDPSSCPGEWLSEPDCTLESVRGPRAQGLPPRRSHQHGPFRGATSFLQHVTGHH

B

ATP Binding Domain -- 17-40 (predicted)

LGKGTGFEVAKGWRRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

IIHADLKPENIML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTGFEVAKGWRRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE
LLEQNLFQKNNFAPLPAHIRTVTLQVLTALARLKEIAIHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHFFK
RNPHPDAAANPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSSVASRLTFPDREALAEHADLKSMVELIKRMLTW
ESHERISPSAALRHPFV

FIGURE 3

A

Protein Sequence of Mouse HIPK4

Total length -- 616 AA

MATIQSETDCYDIIIEVLGKGTGFEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFH
DALKFYLVFELLEQNLFQKNNFAPLPAHIRTVTTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFG
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH
AARKAHFFKRNPHPDATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSM
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHEATRYYQLSLRGCRSLQVDGKPPPPVIAAEDGPPYYRLAEEE
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWSDTRADMVSDMLVPLKVASTSHRVPDSGPEPILAFYG
SRLTGRHKARKAPAGSKSDSNFSNLIRLSQASPEDAGPCRGSGWEEGEGRTTSTEPSVIPQREGDGPGIKDRPMDAERPG
PELFDPPSSCPGEWLSEPEWTLLEGIRGSRAQGLPAHHPHPHGPPRTTTSFLQHVGGHH

B

ATP Binding Domain -- 17-40 (predicted)

LGKGTGFEVAKGWRRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

I IHADLKPENIML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTGFEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE
LLEQNLFQKNNFAPLPAHIRTVTTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHFFK
RNPHPDATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSMVELIKRMLTW
ESHERISPSAALRHPFV

FIGURE 4

A

Protein Sequence of Monkey HIPK4

Total length -- 616 AA

MATTQSETDCYDIIIEVLGKGTfGEVAKGWRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFH
DALKFYLVFELLEQNLFQKNNFAPLPARHIRTVTLQVLRALARLKLAI IHADLKPENIMLVDQTRCPFRVKVIDFG
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMaelHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH
AARKAHFFKRNPHPDaanPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSVASRLTFPDREALAEHADLKSM
VELIKRMLTWESHERISPSAALRHPFVSMQQLRNAHETTHYYQLSLRSYRLSLQVEGKPPAPVVAEDGTPYYRLAEEKE
AAGMGSVASSSPFFREEKAPGMQRAIDQLDDLSLQEAGHGLWGETCTDVVSDMMAPLKAAITGRHMPDSGPEPILAFYSS
RLAGRHKARKPPAGSKSDSNLSNLI RLSQVSPEDDRPCRGSSWEEGEHLGASAEPPAILQRDGDGPNIDNMTMEAERPDP
ELFDPSSCPGEWLSEPDWTLEGVRGPRAQGLPPRRSHQHGPARGATSFLQHVTGHH

B

ATP Binding Domain -- 17-40 (predicted)

LGKGTfGEVAKGWRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

IIHADLKPENIML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTfGEVAKGWRSTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE
LLEQNLFQKNNFAPLPARHIRTVTLQVLRALARLKLAI IHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMaelHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHFFK
RNPHPDaanPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSVASRLTFPDREALAEHADLKSMVELIKRMLTW
ESHERISPSAALRHPFV

FIGURE 5

A

Protein Sequence of Rat HIPK4

Total length -- 616 AA

MATIQSETDCYDIIIEVLGKGTFGGEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFH
DALKFYLVFELLEQNLFQKNNFAPLPARHIRTVTTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFG
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH
AARCAHHFFKRNPDPATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSM
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHEATRYYQLSLRGCRLSLQVDGKPPPPVIAAEDGPPYYRLAEEE
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWSDTRADMVSDMLVPLKVASTSHRVPDSGPEPILAFYG
SRLTGRHKARKAPAGSKSDSNFSNLIRLSQASPEDAGPCRGSGWEEGEGRTTSTEPSVIPQREGDGPPIKDRPMDAERPG
PELFDPPSSCPGEWLSEPEWTLEGIRGSRAQGLPAHHHPHGPRTTTSFLQHVGGHH

B

ATP Binding Domain -- 17-40 (predicted)

LGKGTFGGEVAKGWRRSTGEMVAIK

C

Serine/Threonine Binding Domain -- 132-144 (predicted)

I IHADLKPENIML

D

Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTFGGEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE
LLEQNLFQKNNFAPLPARHIRTVTTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARCAHHFFK
RNPDPATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSMVELIKRMLTW
ESHERISPSAALRHPFV

FIGURE 6

A

CLUSTAL W multiple sequence alignment results

MSF: 346 Type: P Check: 4900 ..

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Name: mushipk3_np_034564.kd.pep oo Len: 346 Check: 9189 Weight: 7.5
Name: rathipk3_np_113975.kd.fas.pep oo Len: 346 Check: 347 Weight: 6.5
Name: humhipk3_np_005725.kd.pep oo Len: 346 Check: 9094 Weight: 7.8
Name: humhipk1-like_ax318266.kd.pep oo Len: 346 Check: 773 Weight: 6.8
Name: mushipk1_np_034562.kd.pep oo Len: 346 Check: 878 Weight: 7.0
Name: humhipk2_np_073577.kd.fas.pep oo Len: 346 Check: 11 Weight: 6.7
Name: mushipk2_np_034563.kd.pep oo Len: 346 Check: 1047 Weight: 7.7
Name: wormf20b6_q19632.kd.pep oo Len: 346 Check: 9639 Weight: 16.4
Name: humhipk4.kd.fas.pep oo Len: 346 Check: 4355 Weight: 5.4
Name: monkeyhipk4_ab074449.kd.fas.pe oo Len: 346 Check: 4346 Weight: 5.3
Name: mushipk4.kd.fas.pep oo Len: 346 Check: 5897 Weight: 5.4
Name: rathipk4_xp_218355.kd.fas.pep oo Len: 346 Check: 5822 Weight: 4.8
Name: yeastyak1_np_012394.kd.fas.pep oo Len: 346 Check: 3415 Weight: 12.2
Name: dmcg17090_q95tg3.kd.pep oo Len: 346 Check: 87 Weight: 26.0
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1
mushipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
rathipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk1-lik YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
mushipk1_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk2_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
mushipk2_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
wormf20b6_q1 YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk4.kd. YDIEVLGKG TFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
monkeyhipk4_ YDIEVLGKG TFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
mushipk4.kd. YDIEVLGKG TFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
rathipk4_xp_ YDIEVLGKG TFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
yeastyak1_np_ YLVDILGQG TFGQVVKCQN LLTKEILAVK VVKSRTYLT QSITEAKILE
dmcg17090_q9 ...YIFNCLD DIGQVNVPTD LEGGQLLAEK TDRREFIDLL KRMLTIDQER

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51
mushipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
rathipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk1-lik RLSTENA..D EYNFVRSYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
mushipk1_np_ RLSTENA..D EYNFVRSYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk2_np_ RLSTENA..D EYNFVRSYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
mushipk2_np_ RLSTENA..D EYNFVRSYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
wormf20b6_q1 RLSTENA..D EYNFVRSYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk4.kd. CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF FQKNNFAPL
monkeyhipk4_ CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF FQKNNFAPL
mushipk4.kd. CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF FQKNNFAPL
rathipk4_xp_ CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF FQKNNFAPL
yeastyak1_np_ LLNQKIDPTN KHHFLRMYS FVHKHNLCLV FELLNNLYE LLKQNKFHGL
dmcg17090_q9 RLTPAEALNH SFTRLTHLVD YVYCINNPKAS VQMMEVCRG DFHTVQAST

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	101		150
mushipk3_np_	PLKVIRPVLQ	QVATALKKLK	SLGLIHADLK
rathipk3_np_	PLKVIRPVLQ	QVATALKKLK	SLGLIHADLK
humhipk3_np_	PLKVIRPILQ	QVATALKKLK	SLGLIHADLK
humhipk1-lik	PLKYIRPILQ	QVATALMKLK	SLGLIHADLK
mushipk1_np_	PLKYIRPILQ	QVATALMKLK	SLGLIHADLK
humhipk2_np_	PLKYIRPVLQ	QVATALMKLK	SLGLIHADLK
mushipk2_np_	PLKYIRPVLQ	QVATALMKLK	SLGLIHADLK
wormf20b6_q1	PLNAIRPILF	QVLTALLKLL	SLGLIHADLK
humhipk4.kd.	PARHIRTVTL	QVLTALARLK	ELAIIHADLK
monkeyhipk4_	PARHIRTVTL	QVLRALARLK	ELAIIHADLK
mushipk4.kd.	PARHIRTVTL	QVLRALARLK	ELAIIHADLK
rathipk4_xp_	PARHIRTVTL	QVLRALARLK	ELAIIHADLK
yeastyak1_np	SIQLIRFTTT	QILDSLCVLK	ESKLIHCDLK
dmcg17090_q9	LVTNFVPSST	ENMTFTINNQ	LTSQVQRLVR
			DGRPLAYEGL
			YQIYNRSVA
	151		200
mushipk3_np_	FGSASHVSKT	..VCSTYLQS	RYYRAPEIIL
rathipk3_np_	FGSASHVSKT	..VCSTYLQS	RYYRAPEIIL
humhipk3_np_	FGSASHVSKT	..VCSTYLQS	RYYRAPEIIL
humhipk1-lik	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL
mushipk1_np_	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL
humhipk2_np_	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL
mushipk2_np_	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL
wormf20b6_q1	FGSASHRSKA	..VTNTYLQS	RYYRAPEIIL
humhipk4.kd.	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL
monkeyhipk4_	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL
mushipk4.kd.	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL
rathipk4_xp_	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL
yeastyak1_np	FGSSCEEART	...VYTYIQS	RFYRAPEIIL
dmcg17090_q9	RQYP.....QTRTDS	FQHQLVSNIL
			CPPSYQTMPS
			PTKHVVVWSA
	201		250
mushipk3_np_	FLGWPLYPGA	LEHDQIRYIS	QTQGLPGEQL
rathipk3_np_	FLGWPLYPGA	LEYDQIRYIS	QTQGLPGEQL
humhipk3_np_	FLGWPLYPGA	LEYDQIRYIS	QTQGLPGEQL
humhipk1-lik	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL
mushipk1_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL
humhipk2_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL
mushipk2_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL
wormf20b6_q1	FLGWPLYPGS	SEYDQIRFII	QTQGLPPTSM
humhipk4.kd.	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL
monkeyhipk4_	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL
mushipk4.kd.	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL
rathipk4_xp_	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL
yeastyak1_np	FLGIPIFPGA	SEYNQLTRII	DTLGYPSSWM
dmcg17090_q9	TMQPPLQVPP	QQYVNVPPVP	SMVEPTSGQR
			MLLTNRVQAS
			GVAWPQTG..

	251					300
mushipk3_np_	.TDMSHSGWR	LKTLEEHEAE	TG.MKSKEAR	KYIFNSLDDI	VHVN.....T	
rathipk3_np_	.TDMSHSGWR	LKTLEEHEAE	TG.MKSKEAR	KYIFNSLDDI	VHVN.....T	
humhipk3_np_	.TDMSHSGWR	LKTLEEHEAE	TG.MKSKEAR	KYIFNSLDDV	AHVN.....T	
humhipk1-lik	.PNLGYPLWR	LKTPEEHELE	TG.IKSKEAR	KYIFNCLDDM	AQVN.....M	
mushipk1_np_	.PNLGYPLWR	LKTPEEHELE	TG.IKSKEAR	KYIFNCLDDM	AQVN.....M	
humhipk2_np_	.TDSPLYLWR	LKTPDDHEAE	TG.IKSKEAR	KYIFNCLDDM	AQVN.....M	
mushipk2_np_	.TDSPLYLWR	LKTPDDHEAE	TG.TKSKEAR	KYIFNCLDDM	AQGN.....M	
wormf20b6_q1	HTNVGGSYR	LKTVEEYEAS	SSTAKSKETR	KYIFNVIDDI	SRVC.....Y	
humhipk4.kd.	.HPDAANPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGSVAS	
monkeyhipk4_	.HPDAANPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGSVAS	
mushipk4.kd.	.HPDATNPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGGAVS	
rathipk4_xp_	.HPDATNPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGGAVN	
yeastyak1_np	.SSSSTQKHR	MKTIEEFCRE	YNIVEKPSKQ	YFKWRKLPDI	IRNYR..YPK	
dmcg17090_q9	RQMALVPSWP	QQAPAHSLIV	DSTPLFNVEE	IYPKHHLNLP	RNDLKKESPA	

	301					346
mushipk3_np_	VMDLEGGDLL	AEKADRREFV	NLLKKMLLID	ADLRITPIET	LNHPFV	
rathipk3_np_	VMDLEGSDLL	AEKADRREFV	SLLKKMLLID	ADLRITPIET	LNHPFV	
humhipk3_np_	VMDLEGSDLL	AEKADRREFV	SLLKKMLLID	ADLRITPAET	LNHPFV	
humhipk1-lik	STDLEGTDM	AEKADRREYI	DLLKKMLTID	ADKRITPLKT	LNHQFV	
mushipk1_np_	STDLEGTDM	AEKADRREYI	DLLKKMLTID	ADKRITPLKT	LNHQFV	
humhipk2_np_	TTDLEGSDML	VEKADRREFI	DLLKKMLTID	ADKRITPIET	LNHPFV	
mushipk2_np_	TTDLEGSDML	VEKADRREFI	DLLKKMLTID	ADKRVTPIET	LNHPFV	
wormf20b6_q1	GFESDPVEHL	CDRIDRQEFV	DVLKKMLVLN	PDFRITPAEG	LESKFV	
humhipk4.kd.	RLTFPDREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV	
monkeyhipk4_	RLTFPDREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV	
mushipk4.kd.	RLSFPDREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV	
rathipk4_xp_	RLSFPDREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV	
yeastyak1_np	SIQNSQELID	QEMQNRECLI	HFLGGVLNLN	PLERWTPQQA	MLHPFI	
dmcg17090_q9	HIIAKGNSYR	VPRHEKKEHQ	QLSPVKKRVK	ESSPPHQQRY	QRAAHV	

B

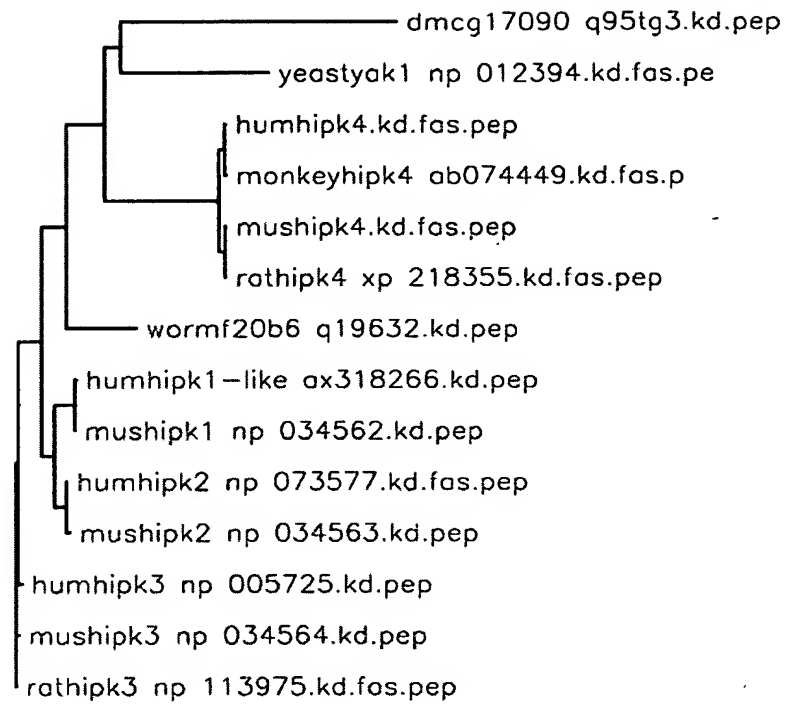


FIGURE 7

A

CLUSTAL W multiple sequence alignment results

MSF: 340 Type: P Check: 1950 ..

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Name: musdyrk1a_np_031916.kd.pep oo   Len: 340 Check: 8276 Weight: 2.2
Name: ratdyrk1a_np_036923.kd.pep oo   Len: 340 Check: 8276 Weight: 2.2
Name: humdyrk1a_np_001387.kd.pep oo   Len: 340 Check: 8161 Weight: 2.2
Name: humdyrk1b_np_004705.kd.pep oo   Len: 340 Check: 7992 Weight: 3.5
Name: musdyrk1b_np_034222.kd.pep oo   Len: 340 Check: 6091 Weight: 2.6
Name: dmmnb_aaf48776.kd.pep oo   Len: 340 Check: 7580 Weight: 5.3
Name: wormt04c10_q22155.kd.pep oo   Len: 340 Check: 9628 Weight: 8.0
Name: dmsmi35a_q9v3d5.kd.pep oo   Len: 340 Check: 6217 Weight: 8.4
Name: humdyrk4_dyr4_human.kd.pep oo   Len: 340 Check: 1420 Weight: 8.0
Name: humdyrk2_np_006473.kd.pep oo   Len: 340 Check: 8233 Weight: 6.6
Name: humdyrk3_np_003573.kd.pep oo   Len: 340 Check: 8166 Weight: 7.5
Name: wormf49e11_q20604.kd.pep oo   Len: 340 Check: 7542 Weight: 7.5
Name: kab7_schpo.kd.pep oo   Len: 340 Check: 9798 Weight: 11.1
Name: pom1_schpo.kd.pep oo   Len: 340 Check: 8379 Weight: 9.8
Name: humhipk4.kd.pep oo   Len: 340 Check: 8285 Weight: 3.5
Name: monkeyhipk4_ab074449.kd.fas.pe oo   Len: 340 Check: 8293 Weight: 3.5
Name: mushipk4.kd.pep oo   Len: 340 Check: 9829 Weight: 3.5
Name: rathipk4_xp_218355.kd.pep oo   Len: 340 Check: 9784 Weight: 3.5

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//

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1
musdyrk1a_np YEIDSLIGKG SFGQVVKAYD RVEQEWVAIK IIKNKKAFLN QAQIEVRLLE
ratdyrk1a_np YEIDSLIGKG SFGQVVKAYD RVEQEWVAIK IIKNKKAFLN QAQIEVRLLE
humdyrk1a_np YEIDSLIGKG SFGQVVKAYD RVEQEWVAIK IIKNKKAFLN QAQIEVRLLE
humdyrk1b_np YEIDSLIGKG SFGQVVKAYD HQTQELVAIK IIKNKKAFLN QAQIELRLLE
musdyrk1b_np YEIDSLIGKG SFGQVVKAYD HQTQELVAIK IIKNKKAFLN QAQIELRLLE
dmmnb_aaf487 YEIDSLIGKG SFGQVVKAYD HEEQCHVAIK IIKNKKPFLN QAQIEVKLLE
wormt04c10_q ILSDTPVGKG SFGQVTKAYD TLNKEEVAIK IIKNKKTFD QAQIEIHLLE
dmsmi35a_q9v YEILEVIGKG SFGQVIRALD HKTNTNTHVAIK IIRNKKRFLN QAVVELNILD
humdyrk4_dyr YEVLKIVIGKG SFGQVAKCLD HKNNELVALK IIRNKKRFHQ QALMELKILE
humdyrk2_np YEVLKIVIGKG SFGQVVKAYD HKVHQHVALK MVRNEKRFHR QAAEEIRILE
humdyrk3_np YEVLKIVIGKG SFGQVARVYD HKLRQYVALK MVRNEKRFHR QAAEEIRILE
wormf49e11_q YEVLKIVIGKG SFGQVIKAFD HKYQQYVALK LVRNEKRFHR QADEEIRILD
kab7_schpo.k YEIIDTVGKG SFGQVLKCID HKRGQVVAIK VIKNRQKFHG QTLVEVGILK
pom1_schpo.k YEIVDFLGKG SFGQVLRCID YETGKLVALK IIRNKKRFHM QALVETKILQ
humhipk4.kd. YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
monkeyhipk4_ YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
mushipk4.kd. YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
rathipk4_xp_ YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
50

```

51

100

musdyrk1a_np	LMNKHDTMCK	YYIVHLKRHF	MFRNHLCLVF	EMLSYNLYDL	LRNTNFRGVS
ratdyrk1a_np	LMNKHDTMCK	YYIVHLKRHF	MFRNHLCLVF	EMLSYNLYDL	LRNTNFRGVS
humdyrk1a_np	LMNKHDTMCK	YYIVHLKRHF	MFRNHLCLVF	EMLSYNLYDL	LRNTNFRGVS
humdyrk1b_np	LMNQHDTEMK	YYIVHLKRHF	MFRNHLCLVF	ELLSYNLYDL	LRNTHFRGVS
musdyrk1b_np	LMNQHDTEMK	YYIVHLKRHF	MFRNHLCLVF	ELLSYNLYDL	LRNTHFRGVS
dmmnb_aaf487	MMNRADAENK	YYIVKLKRHF	MWRNHLCLVF	ELLSYNLYDL	LRNTNFRGVS
wormt04c10_q	LTNAHDKDNK	YNIVTLKGHF	VHRAHLCLVF	ELLSYNLYDL	LKNTSFRGVS
dmsmi35a_q9v	ELREKADAGS	HNVIHMLDYT	YFRKHLCTF	ELMSLNLYEL	IKKNNYNGFS
humdyrk4_dyr	ALRKKDKDNT	YNVVHMKDFF	YFRNHFCITF	ELLGINLYEL	MKNNNFQGF
humdyrk2_np	HLRKQDKDNT	MNVIHMLENF	TFRNHICMTF	ELLSMNLyel	IKKNKFQGF
humdyrk3_np	HLKKQDKTGS	MNVIHMLESF	TFRNHVCMAT	ELLSIDLYEL	IKKNKFQGF
wormf49e11_q	HLRRQSDSGT	HNIIHMLDYF	NFRNHKCITF	ELLSINLYEL	IKRNKFQGF
kab7_schpo.k	RLCEADPADK	NNVIRYLSHF	DFRGHLCIVT	ELLSGNLFDV	IRENNYKGLP
pom1_schpo.k	KIREWDPLDE	YCMVQYTDHF	YFRDHLCVAT	ELLGKNLYEL	IKSNGFKGLP
humhipk4.kd.	CMRGLDPE.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP
monkeyhipk4	CMRGLDPE.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP
mushipk4.kd.	CVRGLDPD.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP
rathipk4_xp	CVRGLDPD.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP

101

150

musdyrk1a_np	LNLTRKFAQQ	MCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
ratdyrk1a_np	LNLTRKFAQQ	MCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
humdyrk1a_np	LNLTRKFAQQ	MCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
humdyrk1b_np	LNLTRKLAQQ	LCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
musdyrk1b_np	LNLTRKLAQQ	LCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
dmmnb_aaf487	LNLTRKFAQQ	LCTALLFLST	PELNIIHCDL	KPENILLCNP	KRS..AIKIV
wormt04c10_q	LNLARKFAQQ	LGKTLLFLSS	PELSIIHCDL	KPENVLLVNA	KRS..QIRVI
dmsmi35a_q9v	MSLIRRFCNS	IVKCLRLLY.	.KENIIHCDL	KPENILLKQR	GSS..SIKVI
humdyrk4_dyr	LSIVRRFTLS	VLKCLQMLS.	.VEKIIHCDL	KPENIVLYQK	GQA..SVKVI
humdyrk2_np	LPLVRKFAHS	ILQCLDALH.	.KNRIIHCDL	KPENILLKQQ	GRS..GIKVI
humdyrk3_np	VQLVRKFAQS	ILQSLDALH.	.KNKIIHCDL	KPENILLKHH	GRS..STKVI
wormf49e11_q	LMLVRKFAYS	MLLCLDLLQ.	.KNRLIHCDL	KPENVLLKQQ	GRS..GIKVI
kab7_schpo.k	LIVVKSFALQ	GLQALRLLO.	.GQNIHCDL	KPENLLLSHP	LKA..RIKLI
pom1_schpo.k	IVVKSITRQ	LIQCLTLLN.	.EKHVIHCDL	KPENILLCHP	FKS..QVKVI
humhipk4.kd.	ARHIRTVTLO	VLTAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI
monkeyhipk4	ARHIRTVTLO	VLRAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI
mushipk4.kd.	ARHIRTVTLO	VLRAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI
rathipk4_xp	ARHIRTVTLO	VLRAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI

	151				200
musdyrk1a_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE
ratdyrk1a_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE
humdyrk1a_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE
humdyrk1b_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGTPYDLAID	MWSLGCILVE
musdyrk1b_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGTPYDLAID	MWSLGCILVE
dmmnb_aaf487	DFGSSCQLGQ	R...IYHYIQ	SRFYRSPEVL	LGIQYDLAID	MWSLGCILVE
wormt04c10_q	DFGSSCQTGH	R...IYQYIQ	SRFYRSPEVL	LGIAYDTKID	MWSLGCILVE
dmsmi35a_q9v	DFGSSCYVDR	K...IYTYIQ	SRFYRSPEVI	LGLQYGT AID	MWSLGCILAE
humdyrk4_dyr	DFGSSCYEHQ	K...VYTYIQ	SRFYRSPEVI	LGHYPDV AID	MWSLGCITAE
humdyrk2_np	DFGSSCYEHQ	R...VYTYIQ	SRFYRAPEVI	LGARYGMPID	MWSLGCILAE
humdyrk3_np	DFGSSCFEYQ	K...LYTYIQ	SRFYRAPEII	LGSRYSTPID	IWSFRCILAE
wormf49e11_q	DFGSSCFDDQ	R...IYTYIQ	SRFYRAPEVI	LGTKYGMPID	MWSLGCILAE
kab7_schpo.k	DFGSSCFYNE	K...VYTYLQ	SRFYRAPEII	LGLEYGKEID	IWSFGCILAE
pom1_schpo.k	DFGSSCFEGE	C...VYTYIQ	SRFYRSPEVI	LGMGYGTPID	VWSLGCIIAE
humhipk4.kd.	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE
monkeyhipk4	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE
mushipk4.kd.	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE
rathipk4_xp	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE

	201				250
musdyrk1a_np	MHTGEPLFSG	ANEVDQMNKI	VEVLGIPPAH	ILDQAPKARK	FFEKLPGDTW
ratdyrk1a_np	MHTGEPLFSG	ANEVDQMNKI	VEVLGIPPAH	ILDQAPKARK	FFEKLPGDTW
humdyrk1a_np	MHTGEPLFSG	ANEVDQMNKI	VEVLGIPPAH	ILDQAPKARK	FFEKLPGDTW
humdyrk1b_np	MHTGEPLFSG	SNEVDQMNRI	VEVLGIPPAH	MLDQAPKARK	YFERLPGGGW
musdyrk1b_np	MHTGEPLFSG	SNEVDQMSRI	VEVLGIPPAP	MLEQAPKARK	YFERLPGGGW
dmmnb_aaf487	MHTGEPLFSG	CNEVDQMNKI	VEVLGMPPKY	LLDQAHKTRK	FFDKIVADGS
wormt04c10_q	MHTGEPLFAG	SSEVDQMMKI	VEVLGMPPKE	MLDIGPKTHK	YFDKTEDGIY
dmsmi35a_q9v	LYTGFPLFPG	ENEVEQLACI	MEVLGLPPKV	LISVARRRRL	FFDSRDAPRC
humdyrk4_dyr	LYTGYPLFPG	ENEVEQLACI	MEVLGLPPAG	FIQTASRRQT	FFDSKGF PKN
humdyrk2_np	LLTGYP LLPG	EDEGDQLACM	IELLGMPSQK	LLDASKRAKN	FVSSKGYPRY
humdyrk3_np	LLTGQPLFPG	EDEGDQLACM	MELLGMPPPK	LLEQSKRAKY	FINSKGIPRY
wormf49e11_q	LLTGYP LLPG	EDENDQLALI	IELLGMPPPK	SLETAKRART	FITSKGYPRY
kab7_schpo.k	LFTGVPLFPG	GNETEQLGYI	MEVLGPPPPMA	LIRNSTRSKA	YFDSEGKPHP
pom1_schpo.k	MYTGFPLFPG	ENEQEQLACI	MEIFGPPDHS	LIDKCSRKKV	FFDSSGKPRP
humhipk4.kd.	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAACKAHH	FFKRNPHPDA
monkeyhipk4	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAARKAHH	FFKRNPHPDA
mushipk4.kd.	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAARKAHH	FFKRNPHPDA
rathipk4_xp	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAARKAHH	FFKRNPHPDA

	251				300
musdyrk1a_np	SLKKT.....K	DGKREYKPPG	TRKLHNILGV	ETGGPGGRRRA
ratdyrk1a_np	SLKKT.....K	DGKREYKPPG	TRKLHNILGV	ETGGPGGRRRA
humdyrk1a_np	NLKKT.....K	DGKREYKPPG	TRKLHNILGV	ETGGPGGRRRA
humdyrk1b_np	TLRRT.....K	ELRKDYQGP	TRRLQEV LGV	QTGGPGGRRRA
musdyrk1b_np	TLRRT.....K	ELR.....
dmmnb_aaf487	YVLKK.....N	QNGRKYKPPG	SRKLHDILGV	ETGGPGGRRRL
wormt04c10_q	YCKKTR....D	GYRHTYKAPG	ARKLHEILGV	TSGGPGGRRRL
dmsmi35a_q9v	ITNT.....KG	RKRSPGSKS.
humdyrk4_dyr	ITNN.....RG	KKRYPDSKD.
humdyrk2_np	CTVTT.....LSDGSV	VLNGGRSRRG	KLRGPPEFRE
humdyrk3_np	CSVTT.....QADGRV	VLVGGRSRRG	KKRGPPGSKD
wormf49ell_q	CTATS.....MPDGSV	VLGARSKR	KMRGPPASRS
kab7_schpo.k	ITDS.....	HNRLLPSTR
pom1_schpo.k	FVSS.....	KGVSRRPFSK
humhipk4.kd.	ANPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	SVASRLTFPD
monkeyhipk4	ANPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	SVASRLTFPD
mushipk4.kd.	TNPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	GAVSRLSFPD
rathipk4_xp	TNPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	GAVNRLSFPD

	301				340
musdyrk1a_np	GESGHTVADY	LKFKDLILRM	LDYDPKTRIQ	PYYALQHSFF	
ratdyrk1a_np	GESGHTVADY	LKFKDLILRM	LDYDPKTRIQ	PYYALQHSFF	
humdyrk1a_np	GESGHTVADY	LKFKDLILRM	LDYDPKTRIQ	PYYALQHSFF	
humdyrk1b_np	GEPGHSPADY	LRFQDLVLRM	LEYEPAARIS	PLGALQHGF	
musdyrk1b_npKDLVLRM	LEYEPAARIS	PLGALQHGF	
dmmnb_aaf487	DEPGHSVSDY	LKFKDLILRM	LDYDPKTRVT	PYYALQHNF	
wormt04c10_q	GEPGHSVEDY	SKFKDLIKRM	LQFDPKQRIS	PYYVVRHPFL	
dmsmi35a_q9v	.LAHILHCQD	RYFIDFLQRC	LEWDPAERMT	PDEAAHHEFL	
humdyrk4_dyr	.LTMVLKTYD	TSFLDFLRRC	LVWEPRLMT	PDQALKHAWI	
humdyrk2_np	WGNALKGCD	PLFLDFLKQC	LEWDPAVRMT	PGQALRHPWL	
humdyrk3_np	WGTALKGCD	YLFIEFLKRC	LHWDPSARLT	PAQALRHPWI	
wormf49ell_q	WSTALKNMGD	ELFVDFLRRC	LDWDPETRMT	PAQALKHKWL	
kab7_schpo.k	TFSQLLNTKQ	ASFLDFLSK	LKWDPKDRIT	VDSALQHEFI	
pom1_schpo.k	SLHQVLQCKD	VSFLSFISDC	LKWDPPERMT	PQQAAQHDFL	
humhipk4.kd.	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	
monkeyhipk4	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	
mushipk4.kd.	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	
rathipk4_xp	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	

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